

IGF1 IS ASSOCIATED WITH GENETIC VARIATION IN KEY PRODUCTION TRAITS IN YOUNG ANGUS CATTLE

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Recent results show circulating levels of insulin-like growth factor-1 (IGF1) are genetically associated with growout and finishing performance of beef cattle and may prove useful as a genetic predictor of carcass and feed efficiency traits (Johnston *et al.* 2001). This paper presents evidence for genetic associations of IGF1 with growth, feed efficiency, fatness and maternal traits in young Angus cattle.

The Angus bull and heifer calves used were born in 1998 and 1999 at the NSW Agricultural Research Centre, Trangie NSW. Following weaning, individual animal average daily gain (ADG), daily feed intake (AFI), residual feed intake (RFI) and feed conversion ratio (FCR) were measured over a standardised 70-day test. At the end of the test subcutaneous fat depth at the 12/13th rib (RIBFAT) and P8 rump (RUMPFAT) sites were measured ultrasonically, and blood sample collected from the tail vein. Plasma was stored frozen and despatched to Primegro Ltd, Adelaide SA, for measurement of IGF1 by ELISA. Estimated Breeding Values (EBVs) for the above production traits plus the individual and maternal components of birth weight (BWT and BWT-M), 200-day weight (200WT and 200WT-M) and 400-day weight (400WT and 400WT-M) were calculated using a best linear unbiased prediction animal model and genetic parameter estimates reported by Arthur *et al.* (2001). Differences between sire progeny groups were taken as evidence for genetic variation in IGF1 and were determined using a GLM procedure with fixed effects of birth year, sex and sire in the final model. Covariation in circulating level of IGF1 with genetic variation in production traits, as measured by EBVs, was determined using a GLM model that included birth year, sex, EBV and EBV-by-sex. Statistically significant regression coefficients for IGF1 with EBVs were taken as evidence for genetic association. Only sires with 4 or more progeny were used. The dataset contained records for 353 progeny from 27 sires (mean 12 progeny per sire in a year), with 3 sires having progeny born in both birth years.

Table 1. Standard deviations of EBVs and regression coefficients for IGF1 with these EBVs for production characteristics of young Angus bulls and heifers. Units are ng/ml of IGF1 per unit of EBV

ADG	RFI	FCR	RIBFAT	RUMPFAT	BWT	BWT-M	200W	200W-M
0.07kg/day	0.50kg/day	0.44kg/kg	0.79mm	1.12mm	2.1kg	0.5kg	7.8kg	3.8kg
-172**	34**	53***	16*	10*	-5.4*	-28**	-1.8**	-3.7**

* P<0.05; ** P<0.01; *** P<0.001

There were significant (P<0.01) differences between sire progeny LS-means for level of IGF1: from 237±19 (SE) to 341±17 ng/mL (SD of sire means 26 ng/ml). This was evidence for genetic variation in circulating levels of IGF1. Phenotypic variation in levels of IGF1 was associated with genetic variation in ADG, RFI, FCR, RIBFAT, RUMPFAT, BWT and BWT-M, 200W and 200W-M (Table 1). Regression coefficients for IGF1 with EBVs for DFI, 400W and 400W-M did not differ from zero (P>0.05). The direction of the associations were such that selection against IGF1 should lead to increased growth rate and improved feed efficiency, lower subcutaneous fat thickness and improved maternal nutrition to the calf before birth (BWT-M) and after birth (200W-M: milk). The actual genetic correlations with these biological traits should be determined before IGF1 is included in a selection index for genetic improvement of beef cattle.

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